

**BLAST****Basic Local Alignment Search Tool**

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Blast 2 sequences

**gb|AAP41037| (1255 letters)**

Results for:

gb|AAP41037.1 E2 glycoprotein precursor [Severe acute respiratory syndrome-related coronavirus] >gi|30795145|gb|A...(1255aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**

gi|30795145|gb|AAP41037.1|

gi|30795145|gb|AAP41037.1|

**Description**

E2 glycoprotein precursor [Severe acute respiratory syndrome-related coronavirus] >gi|30795145|gb|AAP41037.1|  
spike glycoprotein [SARS coronavirus Tor2]

**Molecule type**

amino acid

**Query Length**

1255

**Subject ID**

15461

**Description**

SID 3 of 10/843656

**Molecule type**

amino acid

**Subject Length**

1255

**Program**

BLASTP 2.2.23+ [Citation](#)

**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

**Reference - compositional score matrix adjustment**

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Multiple alignment](#)

**Search Parameters****Search parameter name Search parameter value**

Program	blastp
Word size	3
Expect value	10
Hitlist size	100
Gapcosts	11,1
Matrix	BLOSUM62
Filter string	F
Genetic Code	1
Window Size	40
Threshold	11
Composition-based stats	2

Karlin-Altschul statistics

**Params Ungapped Gapped**

Lambda	0.321182	0.267
K	0.135961	0.041
H	0.41432	0.14

Results Statistics

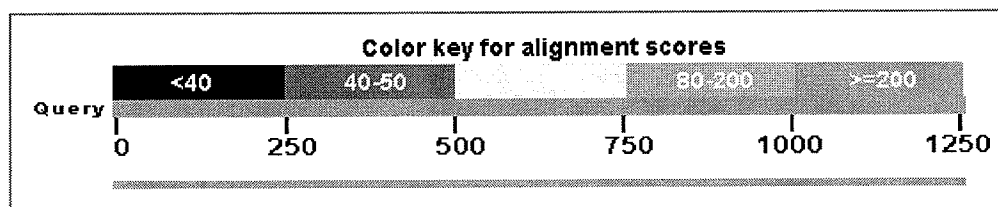
**Results Statistics parameter name Results Statistics parameter value**

Effective search space	1456849
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**Graphic Summary****Distribution of 1 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



[Dot Matrix View](#)

Plot of gi|30795145|gb|AAP41037.1| vs 15461 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: UniGene GEO Gene Structure Map Viewer  
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Links
15461	SID 3 of 10/843656	2600	2600	100%	0.0	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

>lcl|15461 SID 3 of 10/843656  
Length=1255

Score = 2600 bits (6739), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 1254/1255 (99%), Positives = 1255/1255 (100%), Gaps = 0/1255 (0%)

Query	1	MFIFLLFLTTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL	60
Sbjct	1	MFIFLLFLTTLTSGSDDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRSDTLYLTQDLFL	60
Query	61	PFYSNVTGFHTINHTFGNPVIFPKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNS	120
Sbjct	61	PFYSNVTGFHTINHTFGNPVIFPKDGIYFAATEKSNVVRGWVFGSTMNNKSQSVIIINNS	120
Query	121	TNVVIRACNFELCDNPFFAVSKPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Sbjct	121	TNVVIRACNFELCDNPFFAVSKPMGTQHTMIFDNAFNCTFEYISDAFSLDVSEKSGNFK	180
Query	181	HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSP	240
Sbjct	181	HLREFVFKNKDGFYVYKGYQPIDVVRDLPSGFNTLKPFIKPLPLGINITNFRAILTAFSP	240
Query	241	AQDIWGTSAAYFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGIY	300
Sbjct	241	AQDIWGTSAAYFVGYLKPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSFEIDKGIY	300
Query	301	QTSNFRVVPBGDVRFPNITNLCPGEVFNATKFPVYAWERKKISNCVADYSVLYNSTF	360
Sbjct	301	QTSNFRVVPBGDVRFPNITNLCPGEVFNATKFPVYAWERKKISNCVADYSVLYNSTF	360
Query	361	FSTFKCYGVSATKLNLCFSNVYADS FVVKGDVVRQIAPGQTGVIADYNYKLPDDFMGCV	420
Sbjct	361	FSTFKCYGVSATKLNLCFSNVYADS FVVKGDVVRQIAPGQTGVIADYNYKLPDDFMGCV	420
Query	421	LAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPPALNCYWPLND	480
Sbjct	421	LAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPPALNCYWPLND	480
Query	481	YGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLT	540
Sbjct	481	YGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLT	540
Query	541	SSKRFQPFQFGRDVSDFDTSVRDPKTSEILDSPCFGGVSVITPGTNASSEVAVLYQD	600
Sbjct	541	SSKRFQPFQFGRDVSDFDTSVRDPKTSEILDSPCFGGVSVITPGTNASSEVAVLYQD	600
Query	601	VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTAGCLIGAETHVDTSYECDIPIGAGICASY	660
Sbjct	601	VNCTDVSTAIHADQLTPAWRIYSTGNNVFQTAGCLIGAETHVDTSYECDIPIGAGICASY	660
Query	661	HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC	720
Sbjct	661	HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDC	720
Query	721	NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG	780

Sbjct	721	NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG	780
		NMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG	
Query	781	GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFENGL	840
Sbjct	781	GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFENGL	840
Query	841	TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE	900
Sbjct	841	TVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYE	900
Query	901	NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN	960
Sbjct	901	NQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLN	960
Query	961	DILSRDLKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK	1020
Sbjct	961	DILSRDLKVEAEVQIDRLITGRQLSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSK	1020
Query	1021	RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN	1080
Sbjct	1021	RVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFN	1080
Query	1081	GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN	1140
Sbjct	1081	GTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKN	1140
Query	1141	HTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	1200
Sbjct	1141	HTSPDVLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYVWL	1200
Query	1201	GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT	1255
Sbjct	1201	GFIAGLIAIVMVTILLCCMTSCCSCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT	1255

Select All [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#)